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============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=1; day=18; hr=17; min=20; sec=53; ms=127; ]
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Reviewer Comments:
<210> SEQ ID NO 1
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer


Please remove all line headers from the sequence listing, i.e. SEQ ID
NO, LENGTH:, TYPE: ...etc.
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Application No: 10500240   Version No: 2.0

                    Input Set:

                    Output Set:

              Started: 2007-12-28 12:28:19.445
             Finished: 2007-12-28 12:28:24.889
              Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 444 ms
       Total Warnings: 23
         Total Errors: 31
  No. of SeqIDs Defined: 106
     Actual SeqID Count: 106

Error code   Error Description

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W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

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W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

W   213   Artificial or Unknown found in <213> in SEQ ID (15)

W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (17)

W   213   Artificial or Unknown found in <213> in SEQ ID (18)

W   213   Artificial or Unknown found in <213> in SEQ ID (19)

W   213   Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started:	2007-12-28 12:28:19.445
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Total Warnings:	23
Total Errors:	31
No. of SeqIDs Defined:	106
Actual SeqID Count:	106

Error code	Error Description
	This error has occured more than 20 times, will not be displayed
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E 257	Invalid sequence data feature in <221> in SEQ ID (78)
	This error has occured more than 20 times, will not be displayed

<110> APPLICANT: GLYCOFI, INC.

<120> TITLE OF INVENTION: METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE
      STRUCTURES

<130> FILE REFERENCE: GFI/102 PCT

<140> CURRENT APPLICATION NUMBER:10500240

<141> CURRENT FILING DATE:2005-03-23

<150> PRIOR APPLICATION NUMBER: 60/344,169

<151> PRIOR FILING DATE: 2001-12-27

<160> NUMBER OF SEQ ID NOS: 106

<170> SOFTWARE: PatentIn Ver. 2.1

<210> SEQ ID NO 1

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<210> SEQ ID NO 17
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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 18
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<210> SEQ ID NO 19
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<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 23
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 23
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<210> SEQ ID NO 24
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<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (304)..(318)
<223> OTHER INFORMATION: Variable amino acid
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<221> NAME/KEY: MOD_RES

<222> LOCATION: (416)..(436)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 24

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Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
                20                  25                  30
Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
            35                  40                  45
Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
        50                  55                  60
Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65                  70                  75                  80
Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
                85                  90                  95
Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
            100                 105                 110
Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
            115                 120                 125
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
    130                 135                 140
Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145                 150                 155                 160
Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
                165                 170                 175
Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
            180                 185                 190
Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
            195                 200                 205
Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
    210                 215                 220
Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225                 230                 235                 240
Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
            245                 250                 255
Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
            260                 265                 270
His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
            275                 280                 285
Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
    290                 295                 300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
305                 310                 315                 320
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
            325                 330                 335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
            340                 345                 350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
            355                 360                 365
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
    370                 375                 380
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
385                 390                 395                 400
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa
            405                 410                 415
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            420                 425                 430
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            435                 440                 445
Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
        450                 455
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<210> SEQ ID NO 25
<211> LENGTH: 458
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 25

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 1               5                   10                  15
Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
            20                  25                  30
Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
            35                  40                  45
Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
        50                  55                  60
Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 65                  70                  75                  80
Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
                85                  90                  95
Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
            100                 105                 110
Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
            115                 120                 125
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
        130                 135                 140
Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145                 150                 155                 160
Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
                165                 170                 175
Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
            180                 185                 190
Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
            195                 200                 205
Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
        210                 215                 220
Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225                 230                 235                 240
Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
                245                 250                 255
Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
            260                 265                 270
His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
            275                 280                 285
Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
        290                 295                 300
Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
305                 310                 315                 320
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
                325                 330                 335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
            340                 345                 350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
            355                 360                 365
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
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        Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
        385   390   395   400
        Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
                           405   410   415
        Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
                   420   425   430
        Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
                   435   440   445
        Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
                   450   455

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<212> TYPE: PRT
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<221> NAME/KEY: MOD_RES
<222> LOCATION: (333)..(347)
<223> OTHER INFORMATION: Variable amino acid
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        Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu
                   20   25   30
        Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
                       35   40   45
        Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
                 50   55   60
        Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
         65   70   75   80
        His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
                           85   90   95
        His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
                   100   105   110
        Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp
                   115   120   125
        Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val
                   130   135   140
        Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr
        145   150   155   160
        Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu
                           165   170   175
        Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met
                   180   185   190
        Cys Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu Phe
                   195   200   205
        Asn Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu Leu
                   210   215   220
        Leu Ala Gln Arg Trp Gly Trp Gly Ser Leu Ala Leu Val Ile Ser Ala
        225   230   235   240
        Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe
                           245   250   255
        Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile
                   260   265   270
        Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val
                   275   280   285

Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala
        290   295   300
Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln
305   310   315   320
Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa Xaa Xaa Xaa
                    325   330   335